

WE CLAIM:

1. An isolated polynucleotide from coryneform bacteria containing a polynucleotide sequence coding for the sigD gene, selected from the group consisting of
 - a) a polynucleotide that is at least 70% identical to a polynucleotide coding for a polypeptide that contains the amino acid sequence of SEQ ID No. 2,
 - b) a polynucleotide coding for a polypeptide that contains an amino acid sequence that is at least 70% identical to the amino acid sequence of SEQ ID No. 2,
 - c) a polynucleotide that is complementary to the polynucleotides of a) or b), and
 - d) a polynucleotide containing at least 15 successive nucleotides of the polynucleotide sequence of a), b) or c),
2. The polynucleotide according to claim 1, wherein the polypeptide of a) or b) has the activity of the sigma factor D.
3. The polynucleotide according to claim 1, wherein the polynucleotide is a recombinant DNA replicable in coryneform bacteria.
4. The polynucleotide according to claim 1, wherein the polynucleotide is an RNA.
5. The polynucleotide according to claim 3, containing the nucleic acid sequence as shown in SEQ ID No. 1.
6. The polynucleotide according to claim 3, wherein the replicable DNA, comprises
 - (i) the nucleotide sequence shown in SEQ ID No. 1,
or

- (ii) at least one sequence that corresponds to the sequence (i) within the region of degeneracy of the genetic code, or
- (iii) at least one sequence that hybridizes with the sequence that is complementary to the sequence (i) or (ii).
7. The polynucleotide according to claim 6, wherein the replicable DNA, further comprises
- (iv) functionally neutral sense mutations in (i).
8. The polynucleotide according to claim 6, wherein the Hybridisation of sequence (iii) is carried out under conditions of stringency corresponding at most to 2x SSC.
9. The Polynucleotide sequence according to claim 3, that codes for a polypeptide that contains the amino acid sequence shown in SEQ ID No. 2.
10. A Coryneform bacteria, in which the sigD gene is enhanced.
11. The Coryneform bacteria, according to claim 10, wherein the sigD gene is overexpressed.
12. A method for the enzymatic production of L-amino acids, comprising
- a) fermenting, in a medium, coryneform bacteria producing the desired L-amino acid, in which at least the sigD gene or nucleotide sequences coding for the sigD gene are enhanced.
13. The method according to claim 12, wherein the sigD gene or nucleotide sequences coding for the sigD gene are overexpressed.
14. The method according to claim 12, wherein the L-amino

acid is lysine.

15. The method according to claim 12, further comprising
 - b) enriching the L-amino acid in the medium or in the cells of the bacteria.
16. The method according to claim 15, further comprising
 - c) isolating the L-amino acid.
17. The method according to claim 12, wherein bacteria, in which additional genes of the biosynthesis pathway of the desired L-amino acid are enhanced, are used.
18. The method according to claim 12, wherein bacteria, in which the metabolic pathways that reduce the formation of the desired L-amino acid are at least partially switched off, are used.
19. The method according to claim 12, wherein the bacteria have been transformed with a plasmid vector that carries the nucleotide sequence coding for the sigD gene.
20. The method according to claim 12, wherein the expression of the polynucleotide(s) that codes for the sigD gene is enhanced.
21. The method according to claim 20, wherein the polynucleotide(s) that codes for the sigD gene is overexpressed.
22. The method according to claim 12, wherein the regulatory properties of the polypeptide for which the polynucleotide sigD codes are raised.
23. The method according to claim 12, wherein the bacteria being fermented comprise, at the same time, one or more genes which are enhanced; wherein the one or more genes is/are selected from the group consisting of:

the gene dapA coding for dihydrodipicolinate synthase,

the gene gap coding for glyceraldehyde-3-phosphate dehydrogenase,

the gene tpi coding for triosephosphate isomerase,

the gene pgk coding for 3-phosphoglycerate kinase,

the gene zwf coding for glucose-6-phosphate dehydrogenase,

the gene pyc coding for pyruvate carboxylase,

the gene mqo coding for malate-quinone-oxidoreductase,

the gene lysC coding for a feedback-resistant aspartate kinase,

the gene lysE coding for lysine export,

the gene hom coding for homoserine dehydrogenase,

the gene ilvA coding for threonine dehydratase or the allele ilvA(Fbr) coding for a feedback-resistant threonine dehydratase,

the gene ilvBN coding for acetohydroxy acid synthase,

the gene ilvD coding for dihydroxy acid dehydratase, and

the gene zwal coding for the Zwal protein.

24. The method according to claim 12, wherein the bacteria being fermented comprise, at the same time, one or more genes which are attenuated; wherein the one or more genes is/are selected from the group consisting of:

the gene pck coding for phosphoenol pyruvate carboxykinase,

the gene pgi coding for glucose-6-phosphate isomerase,

the gene poxB coding for pyruvate oxidase,

the gene zwa2 coding for the Zwa2 protein.

25. The method according to claim 12, wherein microorganisms of the genus Corynebacterium are used.
26. A Coryneform bacteria containing a vector that carries a polynucleotide according to claim 1.
27. A method for discovering RNA, cDNA, and DNA in order to isolate nucleic acids or polynucleotides or genes that code for the sigma factor D or that have a high degree of similarity to the sequence of the sigD gene, comprising contacting the RNA, cDNA, or DNA with hybridization probes comprising polynucleotide sequences according to claim 1.
28. The method according to claim 27, wherein arrays, micro arrays or DNA chips are employed.